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Tubulin isoform composition tunes microtubule dynamics

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ABSTRACT Microtubules polymerize and depolymerize stochastically, a behavior essential for cell division, motility, and differentiation. While many studies advanced our understanding of how microtubule-associated proteins tune microtubule dynamics in trans, we have yet to understand how tubulin genetic diversity regulates microtubule functions. The majority of in vitro dynamics studies are performed with tubulin purified from brain tissue. This preparation is not representative of tubulin found in many cell types. Here we report the 4.2-Å cryo-electron microscopy (cryo-EM) structure and in vitro dynamics parameters of $\alpha 1\text{B}/\beta\text{I}+\beta\text{IVb}$ microtubules assembled from tubulin purified from a human embryonic kidney cell line with isoform composition characteristic of fibroblasts and many immortalized cell lines. We find that these microtubules grow faster and transition to depolymerization less frequently compared with brain microtubules. Cryo-EM reveals that the dynamic ends of $\alpha 1\text{B}/\beta\text{I}+\beta\text{IVb}$ microtubules are less tapered and that these tubulin heterodimers display lower curvatures. Interestingly, analysis of EB1 distributions at dynamic ends suggests no differences in GTP cap sizes. Last, we show that the addition of recombinant $\alpha 1\text{A}/\beta\text{III}$ tubulin, a neuronal isotype overexpressed in many tumors, proportionally tunes the dynamics of $\alpha 1\text{B}/\beta\text{I}+\beta\text{IVb}$ microtubules. Our study is an important step toward understanding how tubulin isoform composition tunes microtubule dynamics.

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INTRODUCTION

Microtubules are essential dynamic polymers that stochastically switch between polymerization and depolymerization, a behavior known as dynamic instability (Mitchison and Kirschner, 1984; Horio and Hotani, 1986). Dynamic instability is essential for basic cellular processes such as cell division, motility, and differentiation. The building block of the microtubule is the α/β -tubulin heterodimer. Cells use

a diverse repertoire of tubulin dimers to build complex structures with diverse architectures and dynamics to perform these basic cellular functions. Eukaryotes have multiple tubulin isotypes; humans have eight α - and eight β -tubulin isotypes (Redeker, 2010). While some tubulin isoforms are ubiquitously expressed, others are only found in specialized cells such as sperm, neurons, and platelets (Denoulet *et al.*, 1986; Villasante *et al.*, 1986; Wang *et al.*, 1986; Leandro-García *et al.*, 2010). In vivo studies have shown that tubulin isoforms are not functionally interchangeable, suggestive of differential microtubule associate protein (MAPs) recruitment by tubulin isoforms or changes in intrinsic polymer properties (Hoyle and Raff, 1990; Saillour *et al.*, 2014). Tubulin is further functionalized through chemically diverse posttranslational modifications that include glutamylation, glycylation, acetylation, phosphorylation, and amination (Yu *et al.*, 2015).

The majority of in vitro assays are performed with tubulin purified from brain tissue through repeated cycles of polymerization and depolymerization (Weisenberg *et al.*, 1968). While cost-effective, this procedure generates tubulin that is highly heterogeneous, consisting of multiple tubulin isotypes that have chemically diverse and abundant posttranslational modifications (Banerjee *et al.*, 1988; Zambito

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Abbreviations used: AMPPNP, 5' adenylyl- β , γ -imidodiphosphate; cryo-EM, cryo-electron microscopy; GMPCPP, guanylyl-(α , β)-methylene-diphosphonate; PDB, Protein Data Bank.

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et al., 2002). Most importantly, the composition of tubulin isoforms and tubulin posttranslational modifications in these preparations is not representative of that found in most cell types as well as many of the cell lines routinely used in cell biological investigations. Classic studies have reported the characterization of tubulin with less complex compositions purified through polymerization/depolymerization cycles from chicken erythrocytes (Murphy and Wallis, 1983, 1986) and HeLa cells (Newton et al., 2002). A recently introduced affinity purification approach finally enabled the isolation of biochemical amounts of tubulin from various tissues and cell lines (Widlund et al., 2012) that together with recent advances in the expression and purification of pure single isoform human tubulin open a new chapter in the investigation of the biophysical correlates between tubulin sequence, structure, and dynamics (Minoura et al., 2013; Vemu et al., 2016).

Here we purify tubulin from a human embryonic kidney (tsA201) cell line and report its 4.2-Å cryo-electron microscopy (cryo-EM) structure and dynamic parameters. Tubulin purified from this cell line consists predominantly of one α -tubulin isoform, $\alpha 1B$, and two β -tubulin isoforms, βI and βIVb . This β -tubulin composition is characteristic for fibroblasts (Lopata and Cleveland, 1987) as well as cancer cell lines (Rao et al., 2001; Hiser et al., 2006) commonly used for cell biological investigations. In vitro dynamic assays show that these microtubules grow faster and undergo catastrophe less frequently than brain microtubules and cryo-EM reveals structural differences at their dynamic ends. Moreover, we show that microtubule dynamic parameters vary proportionally with the ratio between this nonneuronal tubulin and a recombinantly produced neuronal tubulin isoform that has different dynamic properties. Thus, differential use of tubulin isoforms can have pronounced effects on microtubule structure and dynamics.

RESULTS AND DISCUSSION

In vitro dynamics of human unmodified $\alpha 1B/\beta I+\beta IVb$ tubulin

We purified tubulin from mouse brain and a human embryonic kidney cell line (tsA 201) using a modified tumor overexpressed gene (TOG)-affinity method (Widlund et al., 2012; Vemu et al., 2014) (see *Materials and Methods*) to obtain the purity required for reproducible in vitro dynamics assays. Mass spectrometric analysis shows that tubulin isolated from this cell line contains predominantly unmodified α -tubulin, $\alpha 1B$, and two β -tubulin isoforms, βI and βIVb (Figure 1). To allow a side-by-side comparison, we also purified mouse brain tubulin using the same TOG-based purification procedure (see *Materials and Methods*). Mass spectrometric analysis shows its high level of heterogeneity with more than 30 different separate species consisting of varied α - and β -tubulin isoforms and abundant posttranslational modifications, especially glutamylation.

To examine the dynamics of $\alpha 1B/\beta I+\beta IVb$ tubulin, we performed label-free in vitro dynamic assays using darkfield microscopy (Figure 2). To quantify dynamic parameters, we generated kymographs from time-lapse images of dynamic microtubules (Figure 2A). We find the plus-end growth rates for $\alpha 1B/\beta I+\beta IVb$ microtubules are approximately twofold faster than brain microtubules (Figure 2D). Consistent with this, the plus-end on-rate is $3.7 \text{ dimers s}^{-1} \mu\text{M}^{-1}$ compared with $2.0 \text{ dimers s}^{-1} \mu\text{M}^{-1}$ for brain tubulin (Figure 2C). The plus-end catastrophe frequency (the transition from growth to shrinkage) is approximately twofold lower than that of brain microtubules (Figure 2D). Earlier studies reported HeLa microtubules composed mainly of $\beta I+\beta IVb$ tubulin and an unknown α -tubulin composition undergo catastrophe less than brain microtubules, in agreement with our observations (Newton et al., 2002). The minus-end growth rates and catastrophe frequencies for $\alpha 1B/\beta I+\beta IVb$ microtubules are statistically indistinguishable from brain microtubules (Figure 2E). The dynamic parameters observed for $\alpha 1B/\beta I+\beta IVb$ microtubules are re-

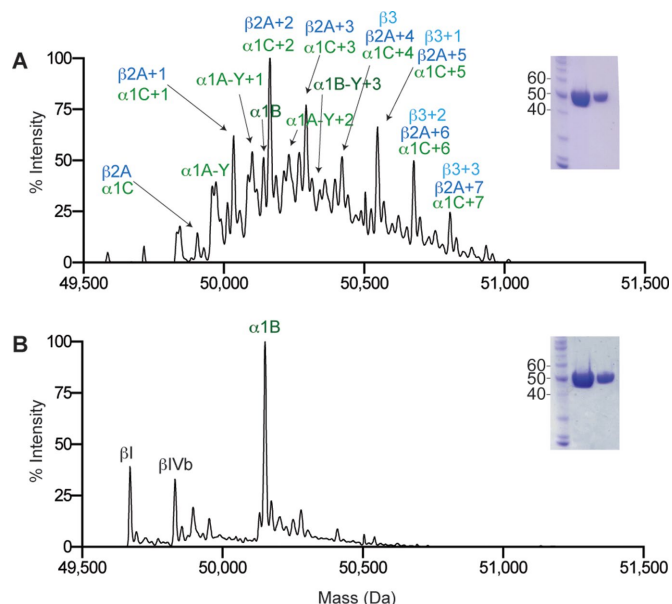


FIGURE 1 Isoform composition and purity of tubulin isolated from brain tissue and tsA201 cells using the TOG affinity method. (A) Mass spectra and SDS-polyacrylamide gel (inset) of tubulin isolated from mouse brain. Number of posttranslationally added glutamates is indicated for the glutamylated species. (B) Mass spectra and SDS-polyacrylamide gel (inset) tubulin isolated from tsA201 cells (see *Materials and Methods*).

producible across multiple purifications from different tsA201 cell growths (Supplemental Figure S1A). Thus, unmodified $\alpha 1B/\beta I+\beta IVb$ microtubules are more stable and reach longer mean lengths than heterogeneous brain microtubules. The $\alpha 1B/\beta I+\beta IVb$ microtubules also undergo catastrophe less frequently than recombinant single isoform $\alpha 1A/\beta III$ microtubules (Vemu et al., 2016). The threefold increase in mean microtubule length from $3.9 \pm 0.3 \mu\text{m}$ to $10.7 \pm 0.6 \mu\text{m}$ for $\alpha 1B/\beta I+\beta IVb$ microtubules is achieved mainly through a combination of catastrophe suppression and polymerization enhancement (Figure 2D). Interestingly, the $\alpha 1B/\beta I+\beta IVb$ microtubules grow threefold faster than the *Saccharomyces cerevisiae* microtubules but have significantly lower catastrophe frequencies (Podolski et al., 2014).

Darkfield imaging allows acquisition at high frame rates that enables the determination of depolymerization rates with high accuracy. These measurements show that $\alpha 1B/\beta I+\beta IVb$ microtubules depolymerize 33% faster than brain microtubules (Figure 2B). The depolymerization rate of $\alpha 1B/\beta I+\beta IVb$ microtubules is also faster than that of neuronal $\alpha 1A/\beta III$ recombinant microtubules ($38.9 \pm 2.3 \mu\text{m/min}$ and $30.5 \pm 1.3 \mu\text{m/min}$ for $\alpha 1B/\beta I+\beta IVb$ and $\alpha 1A/\beta III$ microtubules, respectively [Vemu et al., 2016]). It will be important to establish whether microtubules with different isoform compositions can generate different end depolymerization forces that could be harnessed to move cargo in the cell, such as chromosomes during cell division (Grishchuk et al., 2005).

4.2 Å cryo-EM structure of unmodified $\alpha 1B/\beta I+\beta IVb$ microtubules

To further gain insight into its assembly properties, we determined the structure of $\alpha 1B/\beta I+\beta IVb$ microtubules in the presence of the nonhydrolyzable GTP-analogue guanylyl-(α,β)-methylene-diphosphonate (GMPCPP) using cryoelectron microscopy and single-particle reconstruction (Figure 3A). The overall resolution of the reconstruction is $\sim 4.2 \text{ Å}$ (Supplemental Figure S2A, gold-standard

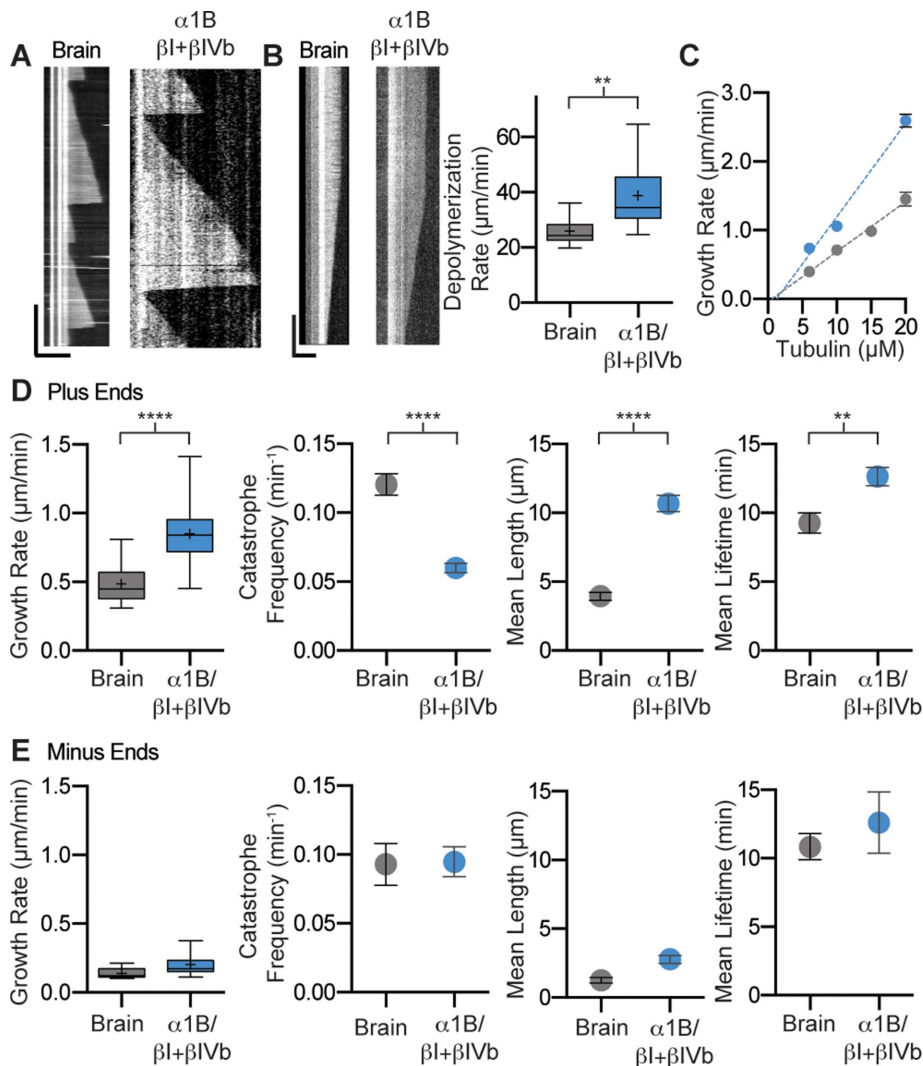


FIGURE 2: Dynamics of brain and $\alpha 1B/\beta 1 + \beta IVb$ microtubules. (A) Kymographs showing typical microtubule growth for brain and $\alpha 1B/\beta 1 + \beta IVb$ tubulin at $6 \mu M$. Horizontal and vertical scale bars, $5 \mu m$ and $5 min$, respectively. (B) Left: kymographs showing a typical depolymerization event for brain and $\alpha 1B/\beta 1 + \beta IVb$ microtubules. Horizontal and vertical scale bars, $5 \mu m$ and $2 s$, respectively. Right: Tukey plot showing plus-end depolymerization rates at $6 \mu M$ tubulin; $n = 12$ and 27 events for brain and $\alpha 1B/\beta 1 + \beta IVb$ microtubules, respectively. (C) Plus-end growth rates as a function of varying tubulin concentration for brain (gray) and $\alpha 1B/\beta 1 + \beta IVb$ microtubules (blue). (D) Plus-end dynamics of brain (gray) and $\alpha 1B/\beta 1 + \beta IVb$ (blue) microtubules at $6 \mu M$ tubulin. From left to right: box-whisker plot (whiskers indicate minimum and maximum) showing plus-end growth rates for brain and $\alpha 1B/\beta 1 + \beta IVb$ microtubules; $n = 38$ and 191 events for brain and $\alpha 1B/\beta 1 + \beta IVb$ tubulin, respectively. Plus-end catastrophe frequencies; $n = 20$ and 69 microtubules for brain and $\alpha 1B/\beta 1 + \beta IVb$ tubulin, respectively. Plus-end microtubule mean lengths; $n = 49$ and 102 events for brain and $\alpha 1B/\beta 1 + \beta IVb$ tubulin, respectively. Plus-end microtubule mean lifetimes; $n = 49$ and 102 events for brain and $\alpha 1B/\beta 1 + \beta IVb$ tubulin, respectively. (E) Minus-end dynamics of brain and $\alpha 1B/\beta 1 + \beta IVb$ tubulin at $6 \mu M$ tubulin. From left to right: box-whisker plot (whiskers indicate minimum and maximum) showing minus-end growth rates for brain and $\alpha 1B/\beta 1 + \beta IVb$ tubulin; $n = 12$ and 84 events for brain and $\alpha 1B/\beta 1 + \beta IVb$ tubulin, respectively. Minus-end catastrophe frequencies; $n = 10$ and 33 microtubules for brain and $\alpha 1B/\beta 1 + \beta IVb$ tubulin, respectively. Minus-end microtubule mean lengths; $n = 9$ and 10 events for brain and $\alpha 1B/\beta 1 + \beta IVb$, respectively. Minus-end microtubule mean lifetimes; $n = 9$ and 10 events for brain and $\alpha 1B/\beta 1 + \beta IVb$, respectively. ** and ****, p values < 0.01 and < 0.0001 , respectively, determined by unpaired t test.

noise-substitution test; Fourier shell correlation 0.143 criterion [Chen *et al.*, 2013]); however, assessment of local resolution suggests that much of the tubulin falls within a higher resolution range ($\sim 3.5 \text{ \AA}$ in more buried regions to $\sim 4.5 \text{ \AA}$ in the most surface exposed

3.3 nm vs. $53.5 \pm 7.3 \text{ nm}$ for $\alpha 1B/\beta 1 + \beta IVb$ and brain [mouse TOG tubulin], respectively). This difference was present regardless of the method used to purify the brain tubulin: commercial bovine brain microtubules (Cytoskeleton) showed a distribution similar to that of

regions; Supplemental Figure S2). At this resolution the pitch of helices, β -strand separation and side-chain densities were apparent and occupancy of nucleotide triphosphate could be seen at both the E- and N-site in $\beta 1 + \beta IVb$ and $\alpha 1B$ -tubulin, respectively (Figure 3, A and B). The structures of microtubules formed from $\alpha 1B/\beta 1 + \beta IVb$ and brain tubulin (previously determined, PDB, 3JAT) are similar. No significant differences were detected at either lateral or longitudinal interfaces between tubulin dimers at this resolution. The dimer repeat distance in GMPCPP $\alpha 1B/\beta 1 + \beta IVb$ microtubules ($83.4 \text{ \AA} \pm 0.1 \text{ \AA}$) was only slightly longer than that in GMPCPP brain microtubules ($83.1 \pm 0.0 \text{ \AA}$), consistent with the presence of an “extended” lattice in microtubules polymerized with this nucleotide analogue (Alushin *et al.*, 2014; Zhang *et al.*, 2015). Despite the lower heterogeneity of this sample compared with brain tubulin (Figure 1) the C-terminal tails and acetylation loop are still unresolved in our reconstruction presumably due to the flexibility of these regions in the absence of effectors as seen in previous reconstructions of both heterogeneous brain microtubules and single-isoform recombinant microtubules (Garnham *et al.*, 2015; Zhang *et al.*, 2015; Vemu *et al.*, 2016).

Dynamic microtubules polymerized with GTP (see *Materials and Methods*) showed similar protofilament distributions for both brain microtubules (mouse purified through the TOG affinity procedure or commercial bovine from Cytoskeleton) and $\alpha 1B/\beta 1 + \beta IVb$ microtubules, with the large majority containing 14 protofilaments and nearly all remaining microtubules containing 13 protofilaments (Supplemental Figure S2, C and D). The ends of dynamic growing microtubules transition from the straight lattice characteristic of the stable polymer to a curved and tapered region where protofilaments are missing, as has been previously described (Mandelkow *et al.*, 1991; Chrétien *et al.*, 1995). This feature was clear in micrographs of polymerizing brain and $\alpha 1B/\beta 1 + \beta IVb$ tubulin (Figure 3C). Measurements of the tapered region for dynamic $\alpha 1B/\beta 1 + \beta IVb$ and brain microtubules revealed a wide distribution from very short ($< 10 \text{ nm}$) to rare but very long ($> 100 \text{ nm}$) end regions for both (Figure 3D). Although the distributions show a large degree of overlap, $\alpha 1B/\beta 1 + \beta IVb$ microtubule tapered ends were shorter than those of brain microtubule populations (Figure 3D; $30.3 \pm$

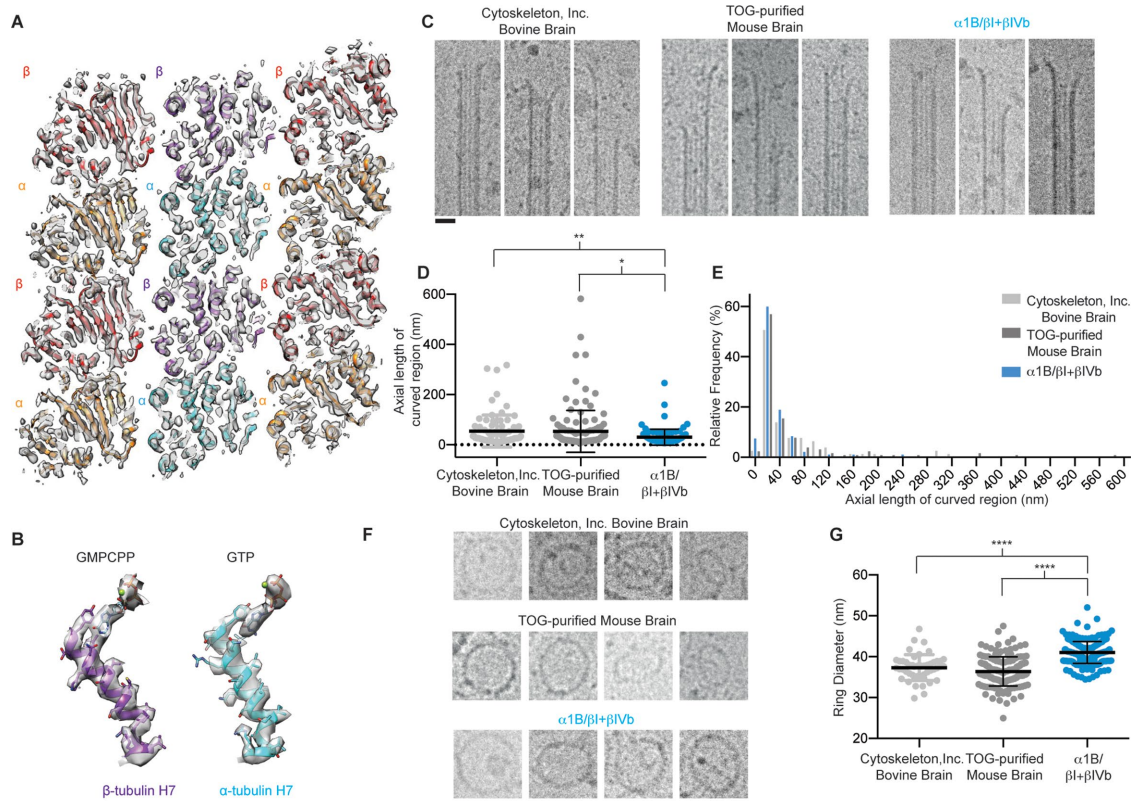


FIGURE 3: Cryoelectron microscopy of $\alpha 1B/\beta I + \beta IVb$ microtubules. (A) Cross-section of the cryo-EM map (gray density) and model of GMPCPP human $\alpha 1B/\beta I + \beta IVb$ microtubules (three protofilaments shown). A central protofilament (PF2) makes lateral contacts with adjacent protofilaments (PF1 and PF3); α -tubulin, orange, β -tubulin, red (PF1, PF3); α -tubulin, cyan; β -tubulin, purple (PF2). (B) β -Tubulin helix H7 and GMPCPP (left, purple) and α -tubulin helix H7 and GTP (right, cyan) and their corresponding experimental densities (gray density). (C) Gallery of polymerizing brain (bovine [Cytoskeleton] and mouse, TOG-affinity purified) and $\alpha 1B/\beta I + \beta IVb$ microtubule ends. Similar architectures are observed, including short and long taper/curved region lengths. Scale bar: 20 nm. (D) Quantification of the length of the curved/tapered region for brain (bovine [Cytoskeleton] and mouse, TOG-affinity purified) and $\alpha 1B/\beta I + \beta IVb$ microtubule ends; $n = 79, 130$, and 95 for mouse brain, bovine brain, and $\alpha 1B/\beta I + \beta IVb$ microtubule ends, respectively. ** and *p value < 0.01 or < 0.05, respectively, as determined by the Mann-Whitney test. (E) Histogram showing curved/tapered region length frequency of $\alpha 1B/\beta I + \beta IVb$ microtubule ends. (F) Gallery of tubulin rings in dynamic preparations of commercial bovine brain (Cytoskeleton) microtubules (top), TOG-affinity purified mouse brain, microtubules (middle), and $\alpha 1B/\beta I + \beta IVb$ microtubules (bottom) showing rings of different diameters and orientations. Scale bar: 20 nm. (G) Quantification of maximum ring diameter from brain (bovine [Cytoskeleton] and mouse, TOG-affinity purified) and $\alpha 1B/\beta I + \beta IVb$ dynamic microtubule preparations; $n = 48, 151$, and 240 for bovine brain, mouse brain, and $\alpha 1B/\beta I + \beta IVb$. **** p value < 0.0001 determined by the Mann-Whitney test.

microtubules assembled from TOG affinity purified mouse brain tubulin (Figure 3D; 53.5 ± 7.3 nm vs. 54.4 ± 7.2 nm). This commercial tubulin also showed similar dynamic parameters to the brain tubulin purified using the TOG affinity approach (Supplemental Figure S1B). In addition, the variance of the tapered ends lengths was lower for $\alpha 1B/\beta I + \beta IVb$ microtubules, with the frequency distribution of $\alpha 1B/\beta I + \beta IVb$ microtubules more skewed toward shorter tapered ends and longer ends for brain microtubules (Figure 3E). The less tapered end architecture of $\alpha 1B/\beta I + \beta IVb$ microtubules could reflect a higher probability of successful incorporation of the more homogeneous $\alpha 1B/\beta I + \beta IVb$ dimers in the microtubule lattice compared with brain tubulin or faster closure of the tapered structures into a complete lattice. The highly heterogeneous mixture of the brain dimers could lead to heterogeneities in the lattice and the pause in growth of some protofilaments, thus the more varied and extreme tapered structures. We note that these measurements were collected from tubulin polymerized at 5 mg/ml in all cases. Future

studies examining taper lengths at a range of tubulin concentrations—which yield different growth rates for each tubulin (Figure 2C)—will more firmly establish the link between the dynamic and structural properties of the ends of these microtubules.

In dynamic microtubule preparations viewed by cryo-EM, a proportion of tubulin “peeling” from depolymerizing microtubule ends closes into rings containing longitudinally associated, curved tubulin dimers (Mandelkow et al., 1991). We observed tubulin rings in micrographs of dynamic $\alpha 1B/\beta I + \beta IVb$ and brain microtubule preparations (Figure 3F). Even though shapes, sizes and orientations of rings in two-dimensional cryo-EM images projections vary, the longest wall-to-wall distance in the rings provides a measure of overall protofilament curvature. Ring diameters for these sets of dynamic microtubules were measured. These showed that $\alpha 1B/\beta I + \beta IVb$ rings are significantly larger on average (41.0 ± 0.2 nm) than those formed by brain tubulin (36.4 ± 0.3 nm and 37.3 ± 0.5 nm for TOG purified and commercial brain tubulin,

respectively) (Figure 3G). Thus, the average tubulin curvature per dimer length (8.2 nm) is 22.8° and 25.8° for α 1B/ β 1+ β IVb and brain tubulin, respectively (Figure 3G). Tubulin dimers need to straighten on incorporation into the microtubule lattice (VanBuren *et al.*, 2002; Wang and Nogales, 2005; Rice *et al.*, 2008). One interpretation of our data is that the energy penalty for straightening the α 1B/ β 1+ β IVb dimers during microtubule incorporation is lower, consistent with their higher polymerization rate. More work on tubulin from different sources will be required to establish this connection.

Similar EB1 distributions on α 1B/ β 1+ β IVb and brain microtubules suggest similar cap sizes

Polymerizing microtubules are protected from depolymerization by a GTP cap at their ends generated by a lag between the GTP hydrolysis rate of the incorporated tubulin and microtubule growth speed. Once the stabilizing cap is “lost,” the microtubule transitions from growth to shrinkage (Carlier, 1982; Mitchison and Kirschner, 1984). Because the α 1B/ β 1+ β IVb microtubules undergo catastrophe less frequently than brain microtubules, we investigated whether there might be a difference in the sizes of their stabilizing GTP caps. The EB1 family of proteins is thought to preferentially bind to the growing microtubule end by sensing the presence of GTP (or GDP-Pi) in the cap structure (Bieling *et al.*, 2007; Kumar and Wittmann, 2012; Maurer *et al.*, 2012). Therefore, it was proposed that the size of the EB1 binding region can be used as a read-out of the GTP cap size (Bieling *et al.*, 2007). We measured EB1-GFP comet lengths at different growth speeds for brain and α 1B/ β 1+ β IVb microtubules (Figure 4). The EB1-GFP comet length increases with increasing microtubule growth speed for brain tubulin, as shown in earlier studies (Bieling *et al.*, 2007). This was also observed for α 1B/ β 1+ β IVb microtubules (Figure 4, A and B). Interestingly, when brain and α 1B/ β 1+ β IVb microtubules are compared at the same growth speeds, the lengths of their EB1-GFP comets are statistically indistinguishable (Figure 4C), suggesting no large differences in their GTP cap sizes. In conclusion, our data indicate that the lower catastrophe frequency and faster growth rates of the α 1B/ β 1+ β IVb microtubules that we observe are due mostly to the large differences between the tubulin on-rates at their dynamic ends and not GTP cap sizes. However, we cannot rule out small differences in GTPase rates not detectable in these assays.

Modulation of α 1B/ β 1+ β IVb tubulin dynamics by a neuronal isoform

β III, a neuronal specific tubulin isoform, is overexpressed in various tumors and has been identified as a strong prognosticator of poor clinical outcomes (Kavallaris, 2010). Its mRNA levels can increase as much as 43- and 71-fold in breast and lung cancers, respectively, when compared with mRNA levels in nontumoral tissues (Leandro-García *et al.*, 2010), and these increases are also manifested in increased β III protein levels (Hiser *et al.*, 2006). β III constitutes 25% of tubulin purified from brain tissue (Banerjee *et al.*, 1988) but is not found in any nonneuronal tissue except on transformation (Leandro-García *et al.*, 2010). To understand the effects of neuronal tubulin on microtubule dynamics in nonneuronal cells, we characterized the dynamic parameters of α 1B/ β 1+ β IVb tubulin in the presence of increasing amounts of recombinant neuronal α 1A/ β III tubulin (Figure 5). We expressed and purified recombinant α 1A/ β III tubulin through a double-selection strategy using an affinity-tag on both α - and β -tubulin. This tubulin is >99.9% homogeneous, has no detectable posttranslational modifications, is free of contamination from endogenous insect tubulins, and is assembly competent (Vemu *et al.*, 2016). We titrated recombinant neuronal α 1A/ β III tubulin into non-neuronal α 1B/ β 1+ β IVb tubulin and measured microtubule dynamics parameters. These show that microtubule dynamic parameters can be tuned by the proportion between these tubulin isoforms (Figure 5 and Supplemental Movie 1). Equimolar amounts of nonneuronal α 1B/ β 1+ β IVb and neuronal α 1A/ β III results in plus-end growth rates comparable to those of α 1A/ β III tubulin alone (Figure 5A) while plus-end catastrophe frequencies are similar to those of neuronal α 1A/ β III alone when threefold molar excess of α 1A/ β III tubulin is added. α 1A/ β III tubulin does not polymerize on its own at the concentrations used; however, we do not know the efficiency of incorporation of the different isoforms into microtubules. At minus ends, α 1B/ β 1+ β IVb and α 1A/ β III microtubules have very similar growth speeds and only a modest difference in catastrophe frequencies. Interestingly, titration of α 1A/ β III does not affect minus-end catastrophe frequency significantly. Our data indicate that α 1A/ β III tubulin is incorporated at the minus ends because 1) at 4 μ M α 1B/ β 1+ β IVb tubulin alone, only ~20% of microtubules exhibit minus-end growth compared with ~60% observed for a combination of 4 μ M α 1B/ β 1+ β IVb and 2 μ M α 1A/ β III tubulin, and 2) α 1B/ β 1+ β IVb and α 1A/ β III tubulin do not polymerize alone at 2 and 4 μ M,

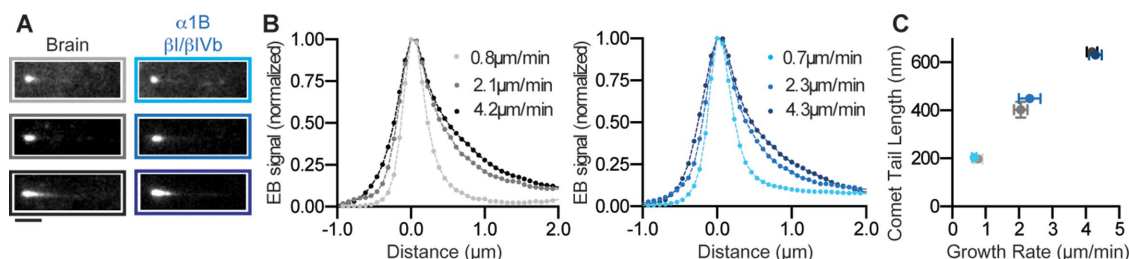


FIGURE 4: EB1-GFP comet analysis on brain and α 1B/ β 1+ β IVb microtubules. (A) TIRF microscopy images of EB1-GFP comets at the ends of growing brain microtubules (left) and α 1B/ β 1+ β IVb (right) microtubules at different growth speeds. From top to bottom: brain microtubule growth speeds are 0.8, 2.1, and 4.2 μ m/min ($n = 26$, 13, and 15 microtubules, respectively). From top to bottom: α 1B/ β 1+ β IVb microtubule growth speeds are 0.7, 2.3, and 4.3 μ m/min ($n = 24$, 12, and 10 microtubules, respectively). Scale bar: 2 μ m. (B) Averaged fluorescence intensity profiles of EB1-GFP comets at different growth speeds of brain (left) and α 1B/ β 1+ β IVb (right) microtubules. $n = 420$, 333, and 421 comet profiles from 12, 13, and 15 brain microtubules at growth speeds of 0.8, 2.1, and 4.2 μ m/min, respectively and $n = 364$, 351, and 234 comet profiles for 15, 12, and 10 α 1B/ β 1+ β IVb microtubules at growth speeds of 0.7, 2.3, and 4.3 μ m/min, respectively. (C) EB1-GFP comet tail lengths as a function of microtubule growth speeds for brain (gray) and α 1B/ β 1+ β IVb (blue) microtubules. Comet tail lengths were obtained by single exponential fits to the averaged intensity profiles (see *Materials and Methods*).

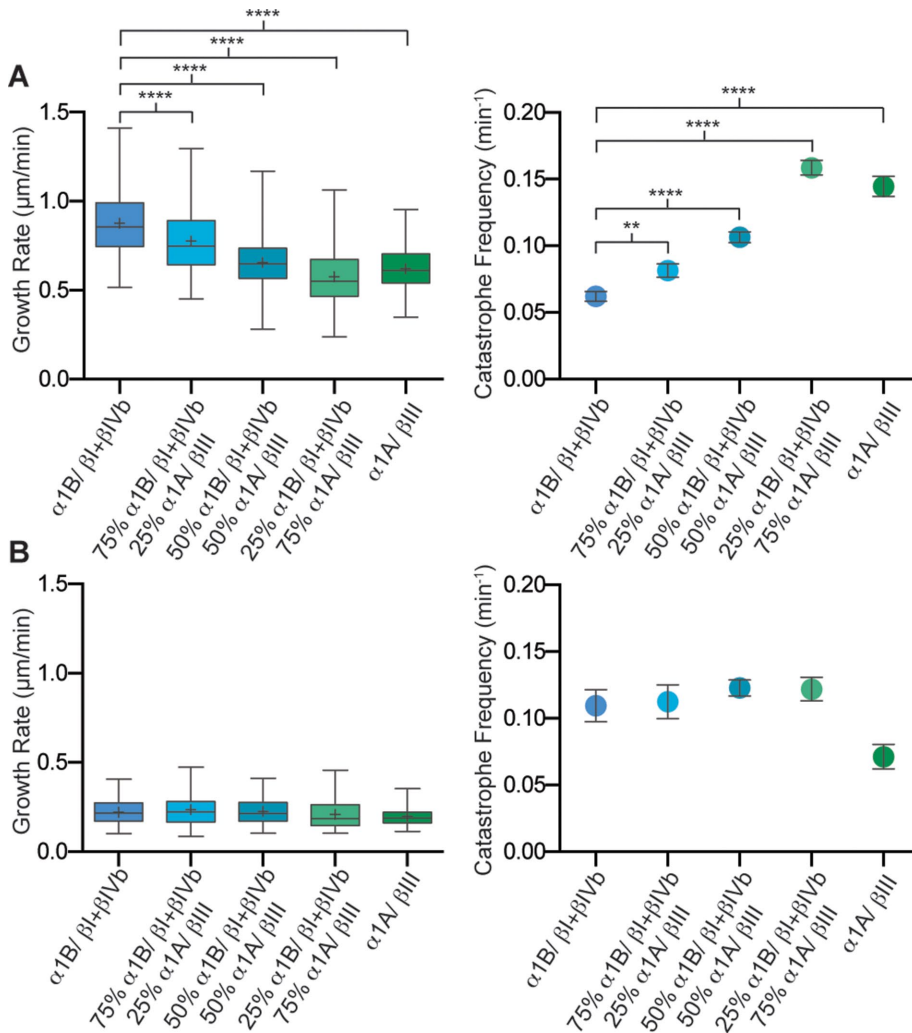


FIGURE 5: Modulation of $\alpha 1B/\beta 1+\beta IVb$ tubulin dynamics by addition of neuronal $\alpha 1A/\beta III$ tubulin. (A) Left panel: box-whisker plot (whiskers indicate minimum and maximum) showing plus-end growth rates at 6 μM tubulin; $n = 191, 258, 432, 377$, and 203 events for $\alpha 1B/\beta 1+\beta IVb$, 75% $\alpha 1B/\beta 1+\beta IVb$ 25% $\alpha 1A/\beta III$, 50% $\alpha 1B/\beta 1+\beta IVb$ 50% $\alpha 1A/\beta III$, 25% $\alpha 1B/\beta 1+\beta IVb$ 75% $\alpha 1A/\beta III$, and $\alpha 1A/\beta III$ tubulin, respectively. Right panel: plus-end catastrophe frequencies; $n = 69, 77, 113, 94$, and 85 microtubules for $\alpha 1B/\beta 1+\beta IVb$, 75% $\alpha 1B/\beta 1+\beta IVb$ 25% $\alpha 1A/\beta III$, 50% $\alpha 1B/\beta 1+\beta IVb$ 50% $\alpha 1A/\beta III$, 25% $\alpha 1B/\beta 1+\beta IVb$ 75% $\alpha 1A/\beta III$, and $\alpha 1A/\beta III$ tubulin, respectively. ** and ****, p values < 0.01 and < 0.0001 , respectively, determined by unpaired t test. (B) Left panel: box-whisker plot (whiskers indicate minimum and maximum) showing minus-end growth rates at 6 μM tubulin; $n = 84, 66, 206, 91$, and 93 events for $\alpha 1B/\beta 1+\beta IVb$, 75% $\alpha 1B/\beta 1+\beta IVb$ 25% $\alpha 1A/\beta III$, 50% $\alpha 1B/\beta 1+\beta IVb$ 50% $\alpha 1A/\beta III$, 25% $\alpha 1B/\beta 1+\beta IVb$ 75% $\alpha 1A/\beta III$, and $\alpha 1A/\beta III$ tubulin, respectively. Right panel: minus-end catastrophe frequencies; $n = 33, 34, 59, 30$, and 40 microtubules for $\alpha 1B/\beta 1+\beta IVb$, 75% $\alpha 1B/\beta 1+\beta IVb$ 25% $\alpha 1A/\beta III$, 50% $\alpha 1B/\beta 1+\beta IVb$ 50% $\alpha 1A/\beta III$, 25% $\alpha 1B/\beta 1+\beta IVb$ 75% $\alpha 1A/\beta III$, and $\alpha 1A/\beta III$ tubulin, respectively.

respectively. The lack of an effect of the $\alpha 1A/\beta III$ tubulin on minus-end dynamics could be due to either the less-efficient incorporation of this isoform at minus ends than plus ends when compared with $\alpha 1B/\beta 1+\beta IVb$ tubulin or to genuine differences in the effects of $\alpha 1A/\beta III$ incorporation between minus and plus ends. These experiments also indicate that overexpression of the $\alpha 1A/\beta III$ tubulin isoform in tumors can significantly alter global microtubule dynamics, with the differences observed being comparable to those elicited by some MAPs such as mitotic centromere-associated kinesin (MCAK) (Walczak et al., 1996), cytoplasmic linker associated proteins (CLASPs) (Al-Bassam et al., 2010), or targeting protein for Xklp2 (TPX2) (Roostalu et al., 2015), but not as dramatic as seen for

Xenopus microtubule-associated protein 215 (XMAP215) (Brouhard et al., 2008), for example. A destabilizing effect of neuronal βIII tubulin was also observed recently when mixed with recombinant βII tubulin in the presence of an unknown α -tubulin composition that included insect α -tubulin (Pamula et al., 2016), as well as in earlier experiments with brain microtubules depleted of βIII tubulin by immunoaffinity chromatography (Panda et al., 1994).

In conclusion, the majority of in vitro dynamics studies performed use heterogeneous scrambled brain microtubules with isoform composition and posttranslational modifications that are not representative of the many cell types found in our bodies. Recent work showed strikingly different activities of the *S. cerevisiae* tip tracking protein Stu2p on *S. cerevisiae* microtubules compared with heterogeneous brain microtubules (Podolski et al., 2014), demonstrating the importance of studying the effects of regulators with the physiologically relevant tubulin substrate. Our study reports the cryo-EM structure and in vitro dynamics parameters for unmodified $\alpha 1B/\beta 1+\beta IVb$ tubulin purified from a human embryonic kidney cell line with tubulin composition similar to that found in fibroblasts and many cell lines used for cell biological investigations. $\alpha 1B/\beta 1+\beta IVb$ microtubules have dramatically different dynamic parameters than those of brain microtubules characterized by faster growth rates and lower catastrophe frequencies, consistent with the less tapered morphology of their growing ends. Furthermore, we show that the dynamics of these nonneuronal microtubules can be proportionally tuned by the addition of a neuronal tubulin isoform with different dynamic properties. Thus, in addition to the potential isoform specific recruitment of microtubule regulators, different microtubule dynamics in cells can be elicited by modulating the relative expression levels of tubulin isoforms.

MATERIALS AND METHODS

Affinity purification of tubulin from brain and tsA201 cells

Tubulin from tsA201 cells was purified as previously described (Widlund et al., 2012; Vemu et al., 2014). Briefly, cells were lysed by gentle sonication in 1XBRB80, pH 6.8 (80 mM piperazine-*N,N'*-bis(2-ethanesulfonic acid) [PIPES]), 1 mM $MgCl_2$, 1 mM EGTA, 1 mM dithiothreitol (DTT), and 25 $\mu g/ml$ benzonase. The lysate was cleared by ultracentrifugation at 444,000 $\times g$ for 15 min at 4°C. The homogenate was loaded onto an N-hydroxysuccinimide (NHS)-column (GE Healthcare) coupled to TOG1. The tubulin was eluted with 1XBRB80 supplemented with 0.5 M ammonium sulfate and was buffer exchanged using a PD-10 column (GE Healthcare) into 1XBRB80, 10% glycerol, and 20 μM GTP and was flash frozen in liquid nitrogen. The tubulin was further purified by cycling (Castoldi and Popov,

2003). Tubulin was buffer exchanged using a PD10 column into 1XBRB80 and 20 μ M GTP and flash frozen in liquid nitrogen. Mass spectrometric analysis of this tubulin indicated that it contains one major α -tubulin (α 1B) and two β -tubulin (β I+ β IVb) isoforms. The same protocol was used to affinity purify tubulin from mouse brains. Wild-type C57/BL6 mice were administered CO₂ gas. Their brains were immediately extracted, washed with cold 1XBRB80, pH 6.8, and flash frozen in liquid nitrogen. The brains were thawed on ice and homogenized in 50 mM 2-(N-morpholino)ethanesulfonic acid (Mes), pH 6.6, 1 mM CaCl₂, 1 mM PMSF, and 1 mM DTT using a polytron three times for 5 s each at low pulses and three times for 5 s at high pulses. The lysate was cleared and tubulin was purified as described above.

Purification of recombinant single-isoform human tubulin

Recombinant single-isoform human α 1A/ β III tubulin was expressed using baculovirus and purified as previously described (Vemu et al., 2016). In brief, α 1A with an internal His-tag and β III with a C-terminal cleavable Flag tag was purified using a Ni-NTA column (Qiagen) and anti-flag G1 affinity resin (Gen Script) to ensure no insect tubulin contamination. The tubulin was further purified by ion exchange chromatography using a Resource Q anion exchange column (GE Healthcare). Peak fractions were combined and buffer exchanged into 1XBRB80 supplemented with 20 μ M GTP using a PD10 column.

In vitro microtubule dynamics assays

GMPCPP-stabilized microtubule seeds were prepared as described in Gell et al. (2010). The GMPCPP seeds were immobilized onto neutravidin coated glass as described previously (Szyk et al., 2014). Dynamic assays were performed as described previously (Vemu et al., 2016). The final imaging buffer contained 1XBRB80, pH 6.8, supplemented with 100 mM KCl, 1 mM GTP, 1% pluronic F-127, and oxygen scavengers. An objective heater (Bioptechs) was used to heat the chamber to 30°C. All chambers were sealed and allowed to equilibrate on the microscope stage for 5 min before imaging. Dark-field images were taken once every 5 s. Image acquisition for the determination of accurate depolymerization rates was performed at 40 frames/s. Kymographs were generated from darkfield images using the Multi Kymograph Plugin in ImageJ. Kymographs were hand traced and dynamic parameters were quantified as previously described (Vemu et al., 2016).

Microtubule cryo-EM sample preparation

α 1B/ β I+ β IVb tubulin was polymerized at 37°C for 45 min at a final concentration of 2.5 mg/ml in BRB80 buffer (80 mM PIPES, 2 mM MgCl₂, 1 mM EGTA, 1 mM DTT) with 1 mM GMPCPP. GMPCPP-bound microtubules were double cycled by depolymerizing GMPCPP microtubules on ice for 5 min then repolymerizing at 37°C for 45 min after adding 2 mM GMPCPP. GMPCPP-bound microtubules were diluted to a final concentration of 2.5 μ M in BRB20 buffer (20 mM PIPES, 2 mM MgCl₂, 1 mM EGTA, 1 mM DTT) and added to glow-discharged C-flat holey carbon grids (Protochips, 2 μ m holes, 4 μ m spacing). Human kinesin-3 motor domain (20 μ M; Kif1A, residues 1–361, see Atherton et al. [2014]) in BRB20 containing 2 mM 5' adenylyl- β , γ -imidodiphosphate (AMPPNP) was applied to the grid, and the sample was blotted and then vitrified in liquid ethane using a Vitrobot (FEI Co.) operating at 25°C and 100% humidity.

Dynamic microtubules were prepared by polymerizing 5 mg/ml α 1B/ β I+ β IVb, bovine brain tubulin (Cytoskeleton) or mouse brain tubulin (TOG-affinity purified) in BRB80 buffer with 1 mM GTP at 37°C for 2 min. The sample was applied to holey carbon grids in a Vitrobot (FEI Co.) operating at 37°C and 70% humidity and allowed

to polymerize for a further minute before blotting and vitrification in liquid ethane.

Data collection and subframe processing for three-dimensional reconstruction

Images of microtubule-kinesin complexes were collected on a FEI Tecnai G2 Polara operating at 300 kV with a DE20 direct electron detector (Direct Electron) with a calibrated magnification of 52,117 \times corresponding to a final sampling of 1.22 \AA /pixel and a defocus range of 0.5–3.5 μ m. A total electron dose of \sim 50e-/ \AA^2 over a 1.5 s exposure and a frame rate of 15 frames/s was used, giving in a total of 23 frames at \sim 2.2e-/ \AA^2 /frame. Subframe processing was performed as described previously (Vemu et al., 2016). In brief, individual \sim 2.2e-/ \AA^2 frames were globally aligned using Imod scripts (Kremer et al., 1996) and then locally aligned using the Optical Flow approach (Abrishami et al., 2015) implemented in Xmipp (de la Rosa-Trevin et al., 2013). The full dose of \sim 50e-/ \AA^2 was used for particle picking and CTF determination in CTFFind3 (Mindell and Grigorieff, 2003), and \sim 25e-/ \AA^2 was used in particle processing to center particles and determine their Euler angles.

Cryo-EM data processing

Data processing was performed as previously described (Vemu et al., 2016). Briefly, straight kinesin-3-decorated 14pf microtubules were manually boxed in Eman Boxer, serving as input for a set of custom-designed semi-automated single-particle processing scripts utilizing Spider and FREALIGN as described previously (Sindelar and Downing, 2007) with minor modifications. The final 14pf microtubule reconstruction was assessed for overfitting during refinement using a high-resolution noise-substitution test (Chen et al., 2013). Using local resolution estimates determined with the blocres program in Bsoft, the reconstruction was sharpened with a Bfactor of \sim 180 up to a resolution of 5.5 or 4 \AA for visualization of kinesin or tubulin densities respectively.

Cryo-EM model building and refinement

α 1B/ β I tubulin was built directly into density in Coot (Emsley et al., 2010) using the recently solved high-resolution cryo-EM model of the brain tubulin 14pf GMPCPP microtubule (PDB 3JAT [Zhang et al., 2015]) as a starting model. After model building, real-space refinement with symmetry restraints was performed in Phenix followed by refinement with symmetry restraints in REFMAC v5.8 modified for cryo-EM data (Supplemental Table 1) (Brown et al., 2015). Secondary structure and reference restraints used with REFMAC based on the high-resolution tubulin crystal structure PDB 4DRX (Pecqueur et al., 2012) were generated with ProSMART (Nicholls et al., 2012).

Protofilament number, ring, and end-length quantification

Using a FEI Tecnai T12 operating at 120 kV and a 4kx4k charge-coupled device (CCD) camera (Gatan) images of dynamic brain or α 1B/ β I+ β IVb tubulin microtubules were collected. A defocus range of 2–4 μ m, a total dose of 30e- over a 1 s exposure, and low pass/Fourier filtering was used to allow visualization of moiré patterns and thereby assign the microtubule protofilament and helical start number (Ray et al., 1993). Ring diameters in these dynamic samples were quantified only for closed single rings using straight line and “measure” in FIJI (Schindelin et al., 2012) from the longest edge-to-edge distance in rings imaged at different projection angles. The axial length of curved end regions in dynamic microtubule preparations were also measured using straight line and “measure” in FIJI by drawing a straight line continuing along the microtubule axis

from the start of the curved/tapered region to the microtubule extreme end.

EB1-GFP tip tracking

Human full-length EB1 fused to a C-terminal GFP-tag was purified using a Ni-affinity column. The final concentration of EB1 in the experiments was 100 nM. Comets were analyzed to determine the average decay length of the GFP signal on the microtubule. First, ImageJ was used to draw kymographs of growing microtubule tips. These kymographs were then read by a custom-written MATLAB (Mathworks) script. First, the maximum intensity in each line was found and a Gaussian fit to the line profile covering 3 μm of the lattice and extending 2 μm beyond the microtubule tip was performed to find the center of the comet. The location of the center was then subtracted from each data point such that the brightest part of the tip is located at the origin. These steps were repeated for each line in the kymograph. Next, all of the aligned comet profiles were binned into single pixel size bins (77 nm), and their average values were calculated. These data were then plotted in Prism and fitted to a single exponential from the first pixel after the peak to the end of the comet tail. The mean decay length for each comet was determined from the inverse of the exponential decay constant. For all exponential fits, $R^2 > 0.99$.

Accession numbers

The PDB and EMDB accession codes for the GMPCPP $\alpha 1\text{B}/\beta 1 + \beta 1\text{Vb}$ microtubule reconstruction are 5N5N and 3589, respectively, and will be released after publication.

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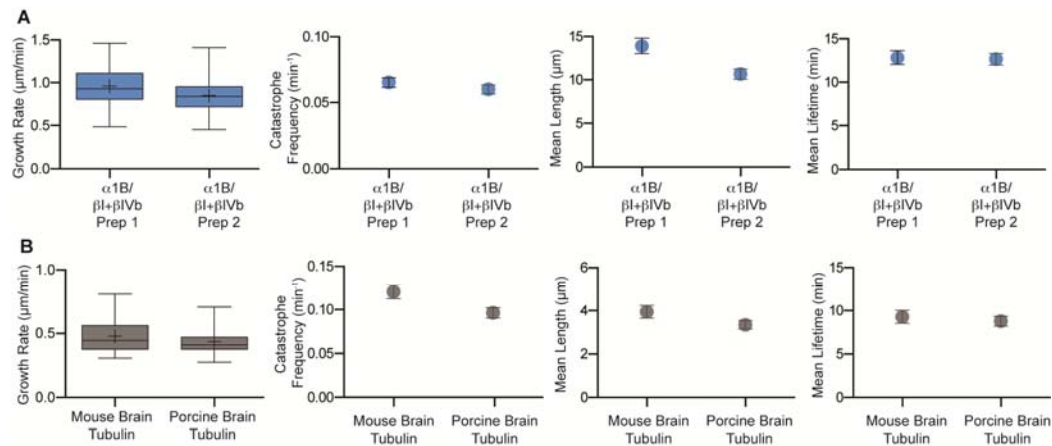
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Supplemental Materials

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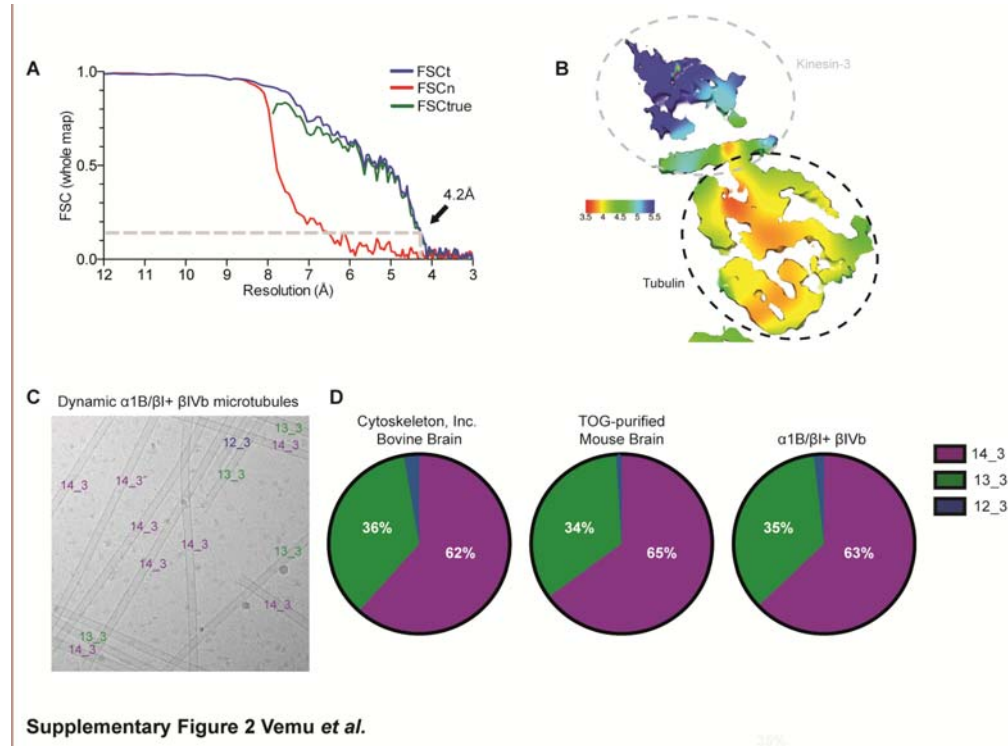
Supplementary Figures



Supplementary Figure 1 Vemu *et al.*

Supplementary Figure 1. Consistent dynamic parameters for $\alpha 1B/\beta I+\beta IVb$ and brain tubulin from different purifications. **(A)** Consistent dynamic parameters for $\alpha 1B/\beta I+\beta IVb$ tubulin from different purifications. *From left to right:* Box-whisker plot (whiskers indicate minimum and maximum) showing plus-end growth rates at $6\mu M$ tubulin from two different tubulin preparations; $n = 246$ and 191 events for purification 1 and purification 2, respectively. Plus-end catastrophe frequencies; $n = 90$ and 69 microtubules. Plus-end microtubule lengths; $n = 74$ and 102 events. Plus-end microtubule lifetimes; $n = 74$ and 102 events for purification 1 and purification 2, respectively. **(B).** Dynamic parameters of mouse brain tubulin purified *via* the TOG affinity approach and commercial brain tubulin (Cytoskeleton Inc.). *From left to right:* Box-whisker plot (whiskers indicate minimum and maximum) showing plus-end growth rates at $6\mu M$ tubulin from the two different tubulin preparations; $n = 38$ and 101 events for mouse brain tubulin and commercial porcine tubulin, respectively. Plus-end catastrophe frequencies; $n = 20$ and 32 microtubules. Plus-end microtubule

lengths; n = 49 and 76 events. Plus-end microtubule lifetimes; n = 49 and 76 events for mouse brain tubulin and commercial tubulin, respectively.



Supplementary Figure 2. Resolution estimates and protofilament number analysis for $\alpha 1B/\beta I + \beta IVb$ microtubules. (A) Utilizing the gold-standard noise substitution method (Chen *et al.*, 2013) the FSC_{true} curve gives an overall resolution estimate of 4.2 Å for the reconstruction of $\alpha 1B/\beta I + \beta IVb$ GMPCPP microtubules bound to kinesin-3. (B) Using the Bsoft program blocres (Cardone *et al.*, 2013) local resolution estimates were calculated and used to color the unfiltered whole reconstruction density. Red density corresponds to 3.5 Å resolution, with a continuum of colors indicating the resolution gradient, ending with blue at 5.5 Å resolution. Tubulin is at a higher resolution, ranging from ~3.5 Å in central regions to ~4.5 Å in more flexible peripheral surface-exposed regions. Kinesin-3, used as a fiducial marker for alignment purposes, is at lower

resolution (resolution of ~5.5 Å) and is excluded from display items. (C) Raw image of dynamic $\alpha 1B/\beta I + \beta IVb$ microtubules. Microtubules are individually labeled with their protofilament number (from 12-14) and start number (3) according to analysis of their Moire patterns (Wade *et al.*, 1990). (D) Quantification of protofilament number distributions for dynamic brain (mouse tubulin purified *via* the TOG approach or commercial bovine brain tubulin (Cytoskeleton Inc.)) or $\alpha 1B/\beta I + \beta IVb$ microtubules polymerized under identical conditions. $n = 73, 200$ and 108 microtubules for bovine brain, mouse brain, and $\alpha 1B/\beta I + \beta IVb$, respectively.

Supplementary Table 1: Refinement statistics and model geometry

Resolution for refinement (Å)	4.2
Map sharpening Bfactor (Å ²)	-180
FSC _{average} ^a	0.72
Rms deviations (bonds)(Å ²)	0.007
Rms deviations (angles)(Å ²)	1.135
Molprobit Score	1.07 (100 th percentile)
Clashscore, all atoms	1.36 (100 th percentile)
Poor rotamers (%)	0.14%
Ramachandran plot favoured (%)	96.70%
Ramachandran outliers (%)	0.24%

^aFSC_{average} = $\Sigma(N_{\text{shell}} \text{FSC}_{\text{shell}}) / \Sigma(N_{\text{shell}})$, where FSC_{shell} is the FSC in a given shell, N_{shell} is the number of structural factors in the shell. FSC_{shell} = $\Sigma(F_{\text{model}} F_{\text{EM}}) / (\sqrt{\Sigma(|F|^2_{\text{model}})} \sqrt{\Sigma(F^2_{\text{EM}})})$